

SEQUENCE LISTING

<110> Sundelin, Johan
Scarborough, Robert M.

<120> Recombinant C140 Receptor, Its Agonists and Antagonists, and
Nucleic Acids Encoding the Receptor

<130> 44481-5006-09-US

<140> US 10/127,691

<141> 2002-04-23

<150> US 08/097,938

<151> 1993-07-26

<150> US 08/390,301

<151> 1995-01-25

<150> US 08/474,414

<151> 1995-06-07

<160> 63

<170> PatentIn Ver. 2.1

<210> 1

<211> 1475

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (232)..(1416)

<223> C140 receptor, genomic DNA and deduced protein
sequences

<400> 1

ccctgtcagt cttaagattc tagaagtcgc tgtcctatac ggaacccaaa actctcactg 60

ttaatgaaat accattgtcg gggcgaagat gtagctcagt ggtaaaatac ttgccagcac 120

acacaagaat tagacttcaa ccgtcaccaa ctgccctgtg taggacggtc ggtcactgaa 180

agagaatatt gtctgcaata ctctaatac atctgtctgt gttcatctga a atg ttc 237
Met Phe

1

cat tta aaa cac agc agc ctt act gtt gga cca ttt atc tca gta atg 285
His Leu Lys His Ser Ser Leu Thr Val Gly Pro Phe Ile Ser Val Met

5

10

15

att ctg ctc cgc ttt ctt tgt aca gga cgc aac aac agt aaa gga aga 333
Ile Leu Leu Arg Phe Leu Cys Thr Gly [Arg Asn Asn Ser Lys Gly Arg]

20

25

30

agt ctt att ggc aga tta gaa acc cag cct cca atc act ggg aaa ggg 381
Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr Gly Lys Gly

35

40

45

50

gtt ccg gta gaa cca ggc ttt tcc atc gat gag ttc tct gcg tcc atc Val Pro Val Glu Pro Gly Phe Ser Ile Asp Glu Phe Ser Ala Ser Ile 55 60 65	429
ctc acc ggg aag ctg acc acg gtc ttt ctt ccg gtc gtc tac att att Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val Val Tyr Ile Ile 70 75 80	477
gtg ttt gtg att ggt ttg ccc agt aat ggc atg gcc ctc tgg atc ttc Val Phe Val Ile Gly Leu Pro Ser Asn Gly Met Ala Leu Trp Ile Phe 85 90 95	525
ctt ttc cga acg aag aag aaa cac ccc gcc gtg att tac atg gcc aac Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met Ala Asn 100 105 110	573
ctg gcc ttg gcc gac ctc ctc tct gtc atc tgg ttc ccc ctg aag atc Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu Lys Ile 115 120 125 130	621
tcc tac cac cta cat ggc aac aac tgg gtc tac ggg gag gcc ctg tgc Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala Leu Cys 135 140 145	669
aag gtg ctc att ggc ttt ttc tat ggt aac atg tat tgc tcc atc ctc Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser Ile Leu 150 155 160	717
ttc atg acc tgc ctc agc gtg cag agg tac tgg gtg atc gtg aac ccc Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val Asn Pro 165 170 175	765
atg gga cac ccc agg aag aag gca aac atc gcc gtt ggc gtc tcc ttg Met Gly His Pro Arg Lys Lys Ala Asn Ile Ala Val Gly Val Ser Leu 180 185 190	813
gca atc tgg ctc ctg att ttt ctg gtc acc atc cct ttg tat gtc atg Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro Leu Tyr Val Met 195 200 205 210	861
aag cag acc atc tac att cca gca ttg aac atc acc acc tgt cac gat Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys His Asp 215 220 225	909
gtg ctg cct gag gag gta ttg gtg ggg gac atg ttc aat tac ttc ctc Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr Phe Leu 230 235 240	957
tca ctg gcc att gga gtc ttc ctg ttc ccg gcc ctc ctt act gca tct Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Leu Leu Thr Ala Ser 245 250 255	1005
gcc tac gtg ctc atg atc aag acg ctc cgc tct tct gct atg gat gaa Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser Ala Met Asp Glu 260 265 270	1053
cac tca gag aac aaa agg cag agg gct atc cga ctc atc atc acc gtg His Ser Glu Lys Lys Arg Gln Arg Ala Ile Arg Leu Ile Ile Thr Val	1101

275	280	285	290	
ctg gcc atg tac ttc atc tgc ttt gct cct agc aac ctt ctg ctc gta				1149
Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro Ser Asn Leu Leu Leu Val	295	300	305	
gtg cat tat ttc cta atc aaa acc cag agg cag agc cac gtc tac gcc				1197
Val His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val Tyr Ala	310	315	320	
ctc tac ctt gtc gcc ctc tgc ctg tgc acc ctc aac agc tgc ata gac				1245
Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys Ile Asp	325	330	335	
ccc ttt gtc tat tac ttt gtc tca aaa gat ttc agg gat cac gcc aga				1293
Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp Phe Arg Asp His Ala Arg	340	345	350	
aac gcg ctc ctc tgc cga agt gtc cgc act gtg aat cgc atg caa atc				1341
Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Asn Arg Met Gln Ile	355	360	365	370
tcg ctc agc tcc aac aag ttc tcc agg aag tcc ggc tcc tac tct tca				1389
Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys Ser Gly Ser Tyr Ser Ser	375	380	385	
agc tca acc agt gtt aaa acc tcc tac tgagctgtac ctgaggatgt				1436
Ser Ser Thr Ser Val Lys Thr Ser Tyr	390	395		
caagcctgct tgatgatgat gatgatgatg gtgtgtgtg				1475
<210> 2				
<211> 395				
<212> PRT				
<213> Mus musculus				
<400> 2				
Met Phe His Leu Lys His Ser Ser Leu Thr Val Gly Pro Phe Ile Ser				
1 5 10 15				
Val Met Ile Leu Leu Arg Phe Leu Cys Thr Gly Arg Asn Asn Ser Lys				
20 25 30				
Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr Gly				
35 40 45				
Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp Glu Phe Ser Ala				
50 55 60				
Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val Val Tyr				
65 70 75 80				
Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly Met Ala Leu Trp				
85 90 95				
Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met				
100 105 110				

Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu
 115 120 125
 Lys Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala
 130 135 140
 Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser
 145 150 155 160
 Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val
 165 170 175
 Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile Ala Val Gly Val
 180 185 190
 Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro Leu Tyr
 195 200 205
 Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys
 210 215 220
 His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr
 225 230 235 240
 Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Leu Leu Thr
 245 250 255
 Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser Ala Met
 260 265 270
 Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile Arg Leu Ile Ile
 275 280 285
 Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro Ser Asn Leu Leu
 290 295 300
 Leu Val Val His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val
 305 310 315 320
 Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys
 325 330 335
 Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp Phe Arg Asp His
 340 345 350
 Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Asn Arg Met
 355 360 365
 Gln Ile Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys Ser Gly Ser Tyr
 370 375 380
 Ser Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr
 385 390 395

<210> 3

<211> 1255

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (56)..(1249)

<223> C140 receptor, genomic DNA and deduced protein sequences

<400> 3

```
cgctccaggc ctgggtgaca gcgagaccct gtctcataaa ttaaaaaatg aataa atg 58
                                                    Met
                                                    1

aat gta ctt tca ttt gaa caa acc agt gtt act gct gaa aca ttt att 106
Asn Val Leu Ser Phe Glu Gln Thr Ser Val Thr Ala Glu Thr Phe Ile
          5                      10                      15

tct. gta atg acc ctt gtc ttc ctt tct tgt aca gga acc aat aga tcc 154
Ser Val Met Thr Leu Val Phe Leu Ser Cys Thr Gly Thr Asn Arg Ser
          20                      25                      30

tct aaa gga aga agc ctt att ggt aag gtt gat ggc aca tcc cac gtc 202
Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val
          35                      40                      45

act gga aaa gga gtt aca gtt gaa aca gtc ttt tct gtg-gat gag ttt 250
Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe
          50                      55                      60                      65

tct gca tct gtc ctc act gga aaa ctg acc act gtc ttc ctt cca att 298
Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Ile
          70                      75                      80

gtc tac aca att gtg ttt gtg gtg ggt ttg cca agt aac ggc atg gcc 346
Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met Ala
          85                      90                      95

ctg tgg gtc ttt ctt ttc cga act aag aag aag cac cct gct gtg att 394
Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile
          100                     105                     110

tac atg gcc aat ctg gcc ttg gct gac ctc ctc tct gtc atc tgg ttc 442
Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe
          115                     120                     125

ccc ttg aag att gcc tat cac ata cat ggc aac aac tgg att tat ggg 490
Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly
          130                     135                     140                     145

gaa gct ctt tgt aat gtg ctt att ggc ttt ttc tat ggc aac atg tac 538
Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr
          150                     155                     160

tgt tcc att ctc ttc atg acc tgc ctc agt gtg cag'agg tat tgg gtc 586
Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val
          165                     170                     175

atc gtg aac ccc atg ggg cac tcc agg aag aag gca aac att gcc att 634
```

Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile	
180 185 190	
ggc atc tcc ctg gca ata tgg ctg ctg att ctg ctg gtc acc atc cct	682
Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile Pro	
195 200 205	
ttg tat gtc gtg aag cag acc atc ttc att cct gcc ctg aac atc acg	730
Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr	
210 215 220 225	
acc tgt cat gat gtt ttg cct gag cag ctc ttg gtg gga gac atg ttc	778
Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe	
230 235 240	
aat tac ttc ctc tct ctg gcc att ggg gtc ttt ctg ttc cca gcc ttc	826
Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe	
245 250 255	
ctc aca gcc tct gcc tat gtg ctg atg atc aga atg ctg cga tct tct	874
Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser	
260 265 270	
gcc atg gat gaa aac tca gag aag aaa agg aag agg gcc atc aaa ctc	922
Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu	
275 280 285	
att gtc act gtc ctg gcc atg tac ctg atc tgc ttc act cct agt aac	970
Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn	
290 295 300 305	
ctt ctg ctt gtg gtg cat tat ttt ctg att aag agc cag ggc cag agc	1018
Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser	
310 315 320	
cat gtc tat gcc ctg tac att gta gcc ctc tgc ctc tct acc ctt aac	1066
His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn	
325 330 335	
agc tgc atc gac ccc ttt gtc tat tac ttt gtt tca cat gat ttc agg	1114
Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg	
340 345 350	
gat cat gca aag aac gct ctc ctt tgc cga agt gtc cgc act gta aag	1162
Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys	
355 360 365	
cag atg caa gta tcc ctc acc tca aag aaa cac tcc agg aaa tcc agc	1210
Gln Met Gln Val Ser Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser	
370 375 380 385	
tct tac tct tca agt tca acc act gtt aag acc tcc tat tgagtt	1255
Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr	
390 395	
<210> 4	
<211> 398	
<212> PRT	

<213> Homo sapiens

<400> 4

Met Asn Val Leu Ser Phe Glu Gln Thr Ser Val Thr Ala Glu Thr Phe
1 5 10 15
Ile Ser Val Met Thr Leu Val Phe Leu Ser Cys Thr Gly Thr Asn Arg
20 25 30
Ser Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His
35 40 45
Val Thr Gly Lys Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu
50 55 60
Phe Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro
65 70 75 80
Ile Val Tyr Thr Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met
85 90 95
Ala Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val
100 105 110
Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp
115 120 125
Phe Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr
130 135 140
Gly Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met
145 150 155 160
Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp
165 170 175
Val Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala
180 185 190
Ile Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile
195 200 205
Pro Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile
210 215 220
Thr Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met
225 230 235 240
Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala
245 250 255
Phe Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser
260 265 270
Ser Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys
275 280 285
Leu Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Thr Pro Ser
290 295 300

Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln
 305 310 315 320
 Ser His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu
 325 330 335
 Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe
 340 345 350
 Arg Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val
 355 360 365
 Lys Gln Met Gln Val Ser Leu Thr Ser Lys Lys His Ser Arg Lys Ser
 370 375 380
 Ser Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
 385 390 395

<210> 5
 <211> 395
 <212> PRT
 <213> Mus musculus

<220>
 <223> Protein sequence of C140 receptor

<400> 5
 Met Phe His Leu Lys His Ser Ser Leu Thr Val Gly Pro Phe Ile Ser
 1 5 10 15
 Val Met Ile Leu Leu Arg Phe Leu Cys Thr Gly [Arg Asn Asn Ser Lys
 20 25 30
 Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr Gly
 35 40 45
 Lys Gly Val Pro Val Glu Pro Gly Phe Ser Ile Asp Glu Phe Ser Ala
 50 55 60
 Ser Ile Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro Val Val Tyr
 65 70 75 80
 Ile Ile Val Phe Val Ile Gly Leu Pro Ser Asn Gly Met Ala Leu Trp
 85 90 95
 Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met
 100 105 110
 Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu
 115 120 125
 Lys Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala
 130 135 140
 Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser
 145 150 155 160

Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val
 165 170 175
 Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile Ala Val Gly Val
 180 185 190
 Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr Ile Pro Leu Tyr
 195 200 205
 Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys
 210 215 220
 His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr
 225 230 235 240
 Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Leu Leu Thr
 245 250 255
 Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg Ser Ser Ala Met
 260 265 270
 Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile Arg Leu Ile Ile
 275 280 285
 Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro Ser Asn Leu Leu
 290 295 300
 Leu Val Val His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val
 305 310 315 320
 Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys
 325 330 335
 Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp Phe Arg Asp His
 340 345 350
 Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Asn Arg Met
 355 360 365
 Gln Ile Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys Ser Gly Ser Tyr
 370 375 380
 Ser Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr
 385 390 395

<210> 6

<211> 398

<212> PRT

<213> Homo sapiens

<220>

<223> Protein sequence from cDNA

<400> 6

Met Asn Val Leu Ser Phe Glu Gln Thr Ser Val Thr Ala Glu Thr Phe
 1 5 10 15

Ile Ser Val Met Ile Leu Val Phe Leu Ser Cys Thr Gly Thr Asn Arg
 20 25 30
 Ser Ser Lys Gly Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His
 35 40 45
 Val Thr Gly Lys Gly Val Ile Val Glu Ile Val Phe Ser Val Asp Glu
 50 55 60
 Phe Ser Ala Ser Val Leu Thr Gly Lys Leu Thr Thr Val Phe Leu Pro
 65 70 75 80
 Ile Val Tyr Ile Ile Val Phe Val Val Gly Leu Pro Ser Asn Gly Met
 85 90 95
 Ala Leu Trp Val Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val
 100 105 110
 Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp
 115 120 125
 Phe Pro Leu Lys Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr
 130 135 140
 Gly Glu Ala Leu Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met
 145 150 155 160
 Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp
 165 170 175
 Val Ile Val Asn Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala
 180 185 190
 Ile Gly Ile Ser Leu Ala Ile Trp Leu Leu Ile Leu Leu Val Thr Ile
 195 200 205
 Pro Leu Tyr Val Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile
 210 215 220
 Thr Thr Cys His Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met
 225 230 235 240
 Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala
 245 250 255
 Phe Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser
 260 265 270
 Ser Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys
 275 280 285
 Leu Ile Val Thr Val Leu Ala Met Tyr Leu Ile Cys Phe Ile Pro Ser
 290 295 300
 Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln
 305 310 315 320
 Ser His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu
 325 330 335

Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe
 340 345 350

Arg Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val
 355 360 365

Lys Gln Met Gln Val Ser Leu Ile Ser Lys Lys His Ser Arg Lys Ser
 370 375 380

Ser Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
 385 390 395

<210> 7

<211> 425

<212> PRT

<213> Mus musculus

<220>

<223> Thrombin receptor

<400> 7

Met Gly Pro Arg Arg Leu Leu Leu Val Ala Ala Cys Phe Ser Leu Cys
 1 5 10 15

Gly Phe Leu Leu Ser Ala Arg Thr Arg Ala Arg Arg Pro Glu Ser Lys
 20 25 30

Ala Thr Asn Ala Thr Leu Asp Pro Arg Ser Phe Leu Leu Arg Asn Pro
 35 40 45

Asn Asp Lys Tyr Glu Pro Phe Trp Glu Asp Glu Glu Lys Asn Glu Ser
 50 55 60

Gly Leu Thr Glu Tyr Arg Leu Val Ser Ile Asn Lys Ser Ser Pro Leu
 65 70 75 80

Gln Lys Gln Leu Pro Ala Phe Ile Ser Glu Asp Ala Ser Gly Tyr Leu
 85 90 95

Thr Ser Ser Trp Leu Thr Leu Phe Val Pro Ser Val Tyr Thr Gly Val
 100 105 110

Phe Val Val Ser Leu Pro Leu Asn Ile Met Ala Ile Val Val Phe Ile
 115 120 125

Leu Lys Met Lys Val Lys Lys Pro Ala Val Val Tyr Met Leu His Leu
 130 135 140

Ala Thr Ala Asp Val Leu Phe Val Ser Val Leu Pro Phe Lys Ile Ser
 145 150 155 160

Tyr Tyr Phe Ser Gly Ser Asp Trp Gln Phe Gly Ser Glu Leu Cys Arg
 165 170 175

Phe Val Thr Ala Ala Phe Tyr Cys Asn Met Tyr Ala Ser Ile Leu Leu
 180 185 190

Met Thr Val Ile Ser Ile Asp Arg Phe Leu Ala Val Val Tyr Pro Met
 195 200 205
 Gln Ser Leu Ser Trp Arg Thr Leu Gly Arg Ala Ser Phe Thr Cys Leu
 210 215 220
 Ala Ile Trp Ala Leu Ala Ile Ala Gly Val Val Pro Leu Val Leu Lys
 225 230 235 240
 Glu Gln Thr Ile Gln Val Pro Gly Leu Asn Ile Thr Thr Cys His Asp
 245 250 255
 Val Leu Asn Glu Thr Leu Leu Glu Gly Tyr Tyr Ala Tyr Tyr Phe Ser
 260 265 270
 Ala Phe Ser Ala Val Phe Phe Phe Val Pro Leu Ile Ile Ser Thr Val
 275 280 285
 Cys Tyr Val Ser Ile Ile Arg Cys Leu Ser Ser Ser Ala Val Ala Asn
 290 295 300
 Arg Ser Lys Lys Ser Arg Ala Leu Phe Leu Ser Ala Ala Val Phe Cys
 305 310 315 320
 Ile Phe Ile Ile Cys Phe Gly Pro Thr Asn Val Leu Leu Ile Ala His
 325 330 335
 Tyr Ser Phe Leu Ser His Thr Ser Thr Thr Glu Ala Ala Tyr Phe Ala
 340 345 350
 Tyr Leu Leu Cys Val Cys Val Ser Ser Ile Ser Ser Cys Ile Asp Pro
 355 360 365
 Leu Ile Tyr Tyr Tyr Ala Ser Ser Glu Cys Gln Arg Tyr Val Tyr Ser
 370 375 380
 Ile Leu Cys Cys Lys Glu Ser Ser Asp Pro Ser Ser Tyr Asn Ser Ser
 385 390 395 400
 Gly Gln Leu Met Ala Ser Lys Met Asp Thr Cys Ser Ser Asn Leu Asn
 405 410 415
 Asn Ser Ile Tyr Lys Lys Leu Leu Thr
 420 425

<210> 8

<211> 7

<212> PRT

<213> Mus musculus

<220>

<223> C140 receptor activation peptide

<400> 8

Arg Asn Asn Ser Lys Gly Arg
 1 - 5

<210> 9
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <400> 9
 Xaa Leu Leu Gly Lys
 1 5

 <210> 10
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140
 antagonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <400> 10
 Xaa Leu Ile Gly Arg
 1 5

 <210> 11
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <220>
 <221> VARIANT
 <222> (1)..(2)
 <223> Xaa at position 1 = 3-mercaptopropionic acid; Xaa
 at position 2 = cyclohexylalanine

 <400> 11
 Xaa Xaa Leu Lys Gly
 1 5

 <210> 12

<211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <220>
 <221> VARIANT
 <222> (1)..(2)
 <223> Xaa at position 1 = 3-mercaptopropionic acid; Xaa
 at position 2 = cyclohexylalanine

 <400> 12
 Xaa Xaa Ile Gly Arg
 1 5

 <210> 13
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <400> 13
 Xaa Leu Leu Gly Lys Lys
 1 5

 <210> 14
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 antagonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <400> 14
 Xaa Leu Ile Gly Arg Lys
 1 5

 <210> 15
 <211> 10

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor antagonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <400> 15
 Xaa Leu Ile Gly Arg Lys Glu Thr Gln Pro
 1 5 10

 <210> 16
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor antagonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 3-mercaptopropionic acid

 <400> 16
 Xaa Leu Leu Gly Lys Lys Asp Gly Thr Ser
 1 5 10

 <210> 17
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor antagonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = (n-pentyl) 2-N-Leu

 <400> 17
 Xaa Ile Gly Arg Lys
 1 5

 <210> 18
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
antagonist

<220>
<221> VARIANT
<222> (1)
<223> Xaa at position 1 = Me-N-(n-pentyl)

<400> 18
Xaa Leu Ile Gly Arg Lys
1 5

<210> 19
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist/immunogen

<400> 19
Ser Lys Gly Arg Ser Leu Ile Gly Arg Leu Glu Thr
1 5 10

<210> 20
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist/immunogen

<400> 20
Ile Ser Tyr His Leu His Gly Asn Asn Trp Val Tyr Gly Glu Ala Leu
1 5 10 15

Cys

<210> 21
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist/immunogen

<400> 21
Gln Thr Ile Tyr Ile Pro Ala Leu Asn Ile Thr Thr Cys His Asp Val
1 5 10 15

Leu Pro Glu Glu Val Leu Val Gly Asp Met Phe Asn Tyr Phe Leu
 20 25 30

<210> 22
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist/immunogen

<400> 22
 His Tyr Phe Leu Ile Lys Thr Gln Arg Gln Ser His Val Tyr Ala
 1 5 10 15

<210> 23
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

<400> 23
 Ser Leu Ile Gly Arg Leu
 1 5

<210> 24
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

<400> 24
 Ser Leu Ile Gly Arg Ala
 1 5

<210> 25
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

<400> 25
 Ser Leu Ile Gly Ala Leu
 1 5

<210> 26
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 26
Ser Leu Ile Ala Arg Leu
1 5

<210> 27
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 27
Ser Leu Ala Gly Arg Leu
1 5

<210> 28
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 28
Ser Ala Ile Gly Arg Leu
1 5

<210> 29
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 29
Ala Leu Ile Gly Arg Leu
1 5

<210> 30
<211> 6

<212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 30
 Ser Phe Phe Leu Arg Trp
 1 5

 <210> 31
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 31
 Arg Asn Asn Ser Ser Lys Gly Arg
 1 5

 <210> 32
 <211> 13
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 32
 Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile Thr
 1 5 10

 <210> 33
 <211> 12
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 33
 Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro Ile
 1 5 10

 <210> 34
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 34
Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro Pro
1 5 10

<210> 35
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 35
Ser Leu Ile Gly Arg Leu Glu Thr Gln Pro
1 5 10

<210> 36
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 36
Ser Leu Ile Gly Arg Leu Glu Thr Gln
1 5

<210> 37
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 agonist

<400> 37
Ser Leu Ile Gly Arg Leu Glu Thr
1 5

<210> 38
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 38
Ser Leu Ile Gly Arg Leu Glu
1 5

<210> 39
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 39
Ser Leu Ile Gly Arg Leu
1 5

<210> 40
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 40
Ser Leu Ile Gly Arg
1 5

<210> 41
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 41
Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His Val Thr
1 5 10

<210> 42
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: C140 receptor
agonist

<400> 42
Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His Val
1 5 10

<210> 43
 <211> 11
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 43
 Ser Leu Leu Gly Lys Val Asp Gly Thr Ser His
 1 5 10

 <210> 44
 <211> 10
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 44
 Ser Leu Leu Gly Lys Val Asp Gly Thr Ser
 1 5 10

 <210> 45
 <211> 9
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 45
 Ser Leu Leu Gly Lys Val Asp Gly Thr
 1 5

 <210> 46
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 46
 Ser Leu Leu Gly Lys Val Asp Gly
 1 5

 <210> 47

<211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 47
 Ser Leu Leu Gly Lys Val Asp
 1 5

 <210> 48
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 48
 Ser Leu Leu Gly Lys Val
 1 5

 <210> 49
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 49
 Ser Leu Leu Gly Lys
 1 5

 <210> 50
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <220>
 <221> VARIANT
 <222> (2)
 <223> Xaa at position 2 = cyclohexylalanine (Cha)

 <400> 50
 Ser Xaa Ile Gly Arg
 1 5

<210> 51
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <220>
 <221> VARIANT
 <222> (2)
 <223> Xaa at position 2 = cyclohexylalanine (Cha)

 <400> 51
 Ser Xaa Leu Gly Lys
 1 5

 <210> 52
 <211> 4
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 2,3-diamino propionic acid
 (2,3-diaP)

 <400> 52
 Xaa Ile Gly Arg
 1

 <210> 53
 <211> 5
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 2,3-diamino propionic acid
 (2,3-diaP)

 <400> 53
 Xaa Leu Leu Gly Lys
 1 5

<210> 54
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 54
 Ser Leu Leu Gly Lys Arg
 1 5

 <210> 55
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <400> 55
 Ser Leu Ile Gly Arg Arg
 1 5

 <210> 56
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 receptor
 agonist

 <220>
 <221> VARIANT
 <222> (2)
 <223> Xaa at position 2= cyclohexylalanine (Cha)

 <400> 56
 Ser Xaa Leu Gly Lys Lys
 1 5

 <210> 57
 <211> 6
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: C140 agonist
 receptor

 <220>
 <221> VARIANT

<222> (2)
 <223> Xaa at position 2 = cyclohexylalanine (Cha)

<400> 57
 Ser Xaa Ile Gly Arg Lys
 1 5

<210> 58
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor agonist

<220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 2,3-diamino propionic acid (2,3-diaP)

<400> 58
 Xaa Leu Ile Gly Arg Lys
 1 5

<210> 59
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: C140 receptor agonist

<220>
 <221> VARIANT
 <222> (1)
 <223> Xaa at position 1 = 2,3-diamino propionic acid (2,3-diaP)

<400> 59
 Xaa Leu Leu Gly Lys Lys
 1 5

<210> 60
 <211> 2732
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (73) .. (1269)
 <223> C140 receptor, cDNA and deduced protein sequences

<400> 60

ccctgtgctc agagtagggc tccgagtttc gaaccactgg tggcggattg cccgcccgcc 60

ccacgtccgg gg atg cga agt ctc agc ctg gcg tgg ctg ctg gga ggt atc 111
Met Arg Ser Leu Ser Leu Ala Trp Leu Leu Gly Gly Ile
1 5 10

acc ctt ctg gcg gcc tgc gtc tcc tgc agc cgg acc gag aac ctt gca 159
Thr Leu Leu Ala Ala Ser Val Ser Cys Ser Arg Thr Glu Asn Leu Ala
15 20 25

ccg gga [cgc aac aac agt aaa gga aga] agt ctt att ggc aga tta gaa 207
Pro Gly [Arg Asn Asn Ser Lys Gly Arg] Ser Leu Ile Gly Arg Leu Glu
30 35 40 45

acc cag cct cca atc act ggg aaa ggg gtt ccg gta gaa cca ggc ttt 255
Thr Gln Pro Pro Ile Thr Gly Lys Gly Val Pro Val Glu Pro Gly Phe
50 55 60

tcc atc gat gag ttc tct gcg tcc atc ctc acc ggg aag ctg acc acg 303
Ser Ile Asp Glu Phe Ser Ala Ser Ile Leu Thr Gly Lys Leu Thr Thr
65 70 75

gtc ttt ctt ccg gtc gtc tac att att gtg ttt gtg att ggt ttg ccc 351
Val Phe Leu Pro Val Val Tyr Ile Ile Val Phe Val Ile Gly Leu Pro
80 85 90

agt aat ggc atg gcc ctc tgg atc ttc ctt ttc cga acg aag aag aaa 399
Ser Asn Gly Met Ala Leu Trp Ile Phe Leu Phe Arg Thr Lys Lys Lys
95 100 105

cac ccc gcc gtg att tac atg gcc aac ctg gcc ttg gcc gac ctc ctc 447
His Pro Ala Val Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu
110 115 120 125

tct gtc atc tgg ttc ccc ctg aag atc tcc tac cac cta cat ggc aac 495
Ser Val Ile Trp Phe Pro Leu Lys Ile Ser Tyr His Leu His Gly Asn
130 135 140

aac tgg gtc tac ggg gag gcc ctg tgc aag gtg ctc att ggc ttt ttc 543
Asn Trp Val Tyr Gly Glu Ala Leu Cys Lys Val Leu Ile Gly Phe Phe
145 150 155

tat ggt aac atg tat tgc tcc atc ctc ttc atg acc tgc ctc agc gtg 591
Tyr Gly Asn Met Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val
160 165 170

cag agg tac tgg gtg atc gtg aac ccc atg gga cac ccc agg aag aag 639
Gln Arg Tyr Trp Val Ile Val Asn Pro Met Gly His Pro Arg Lys Lys
175 180 185

gca aac atc gcc gtt ggc gtc tcc ttg gca atc tgg ctc ctg att ttt 687
Ala Asn Ile Ala Val Gly Val Ser Leu Ala Ile Trp Leu Leu Ile Phe
190 195 200 205

ctg gtc acc atc cct ttg tat gtc atg aag cag acc atc tac att cca 735
Leu Val Thr Ile Pro Leu Tyr Val Met Lys Gln Thr Ile Tyr Ile Pro
210 215 220

gca ttg aac atc acc acc tgt cac gat gtg ctg cct gag gag gta ttg 783

Ala Leu Asn Ile Thr Thr Cys His Asp Val Leu Pro Glu Glu Val Leu
225 230 235

gtg ggg gac atg ttc aat tac ttc ctc tca ctg gcc att gga gtc ttc 831
Val Gly Asp Met Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe
240 245 250

ctg ttc ccg gcc ctc ctt act gca tct gcc tac gtg ctc atg atc aag 879
Leu Phe Pro Ala Leu Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Lys
255 260 265

acg ctc cgc tct tct gct atg gat gaa cac tca gag aag aaa agg cag 927
Thr Leu Arg Ser Ser Ala Met Asp Glu His Ser Glu Lys Lys Arg Gln
270 275 280 285

agg gct atc cga ctc atc atc acc gtg ctg gcc atg tac ttc atc tgc 975
Arg Ala Ile Arg Leu Ile Ile Thr Val Leu Ala Met Tyr Phe Ile Cys
290 295 300

ttt gct cct agc aac ctt ctg ctc gta gtg cat tat ttc cta atc aaa 1023
Phe Ala Pro Ser Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys
305 310 315

acc cag agg cag agc cac gtc tac gcc ctc tac ctt gtc gcc ctc tgc 1071
Thr Gln Arg Gln Ser His Val Tyr Ala Leu Tyr Leu Val Ala Leu Cys
320 325 330

ctg tcg acc ctc aac agc tgc ata gac ccc ttt gtc tat tac ttt gtc 1119
Leu Ser Thr Leu Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val
335 340 345

tca aaa gat ttc agg gat cac gcc aga aac gcg ctc ctc tgc cga agt 1167
Ser Lys Asp Phe Arg Asp His Ala Arg Asn Ala Leu Leu Cys Arg Ser
350 355 360 365

gtc cgc act gtg aat cgc atg caa atc tcg ctc agc tcc aac aag ttc 1215
Val Arg Thr Val Asn Arg Met Gln Ile Ser Leu Ser Ser Asn Lys Phe
370 375 380

tcc agg aag tcc ggc tcc tac tct tca agc tca acc agt gtt aaa acc 1263
Ser Arg Lys Ser Gly Ser Tyr Ser Ser Ser Ser Thr Ser Val Lys Thr
385 390 395

tcc tac tgagctgtac ctgaggatgt caagcctgct tgatgatgat gatgatgatg 1319
Ser Tyr

gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcacccgtgt gtgagtgcgt 1379

ggtagggata caccaacatg gatggggctg tcatttccta tccaagctgt ctgtctctgc 1439

accaatcaca agcatgcagc tctccccagg attgacagaa gcctcctcct ttgcatgaga 1499

acagtcttcc actctgatga aaagcatcag tatcagaaac tgaaacgaac tgagaggagc 1559

ttgttttgtg aaagtgaaga gaagatggag ggtcagtgac ttgcaaaaaa aaccaaccaa 1619

acaaaaacta cacctggcaa gaaggctaag actctctgaa atgcttcctt tttccatctg 1679

gagttcgtct cggccttggt caggacctga ggccctggta gagcttcagt ccagttgatt 1739

gactttacag acttgagaga ggagtgaatg aggagtgaat gaggtccttg gcggcatcct 1799
aaccggctaa cagtggcctt gctggacaat aggattcaga tggctggagt tacattctca 1859
caccatttca tcagaactat tggggatctt gatcaatgtg caggtcctt agcgtcagta 1919
accctgggag ctcagacacg atgggggtga ggggtgggggt gggggtgggg gtgaggctct 1979
acaaacctta gtgatgactg cagacacaga accatggagc tgagcctgct tctgcttgcc 2039
agggcaccac tgtaatgttg gcaaagaaaa accaacagca gtgttttgag cctctttttt 2099
tggtcagttt atgatgaatt tgccatttgg tttattggga ttttcagttc ctttattact 2159
ttgttgtaat tttgtgtgtt tattagtcaa gaaaaagaag atgaggctct taaaaatgta 2219
aataaaattt ttggtttttt ggttttttta cttgggccaa ctacaaatac tgcttagggt 2279
tttttctaac ttaattgtta actacatcat gtgaacttaa gacattttca tgataaagca 2339
ttactgtagt gtcagttttc cctcatcctc gatcatagtc cttcccgta agcaggggccc 2399
ttccctccc cccctttgc cgtttccctc cccaccagat agtccccctg tctgctttaa 2459
cctaccagtt agtattttat aaaaacagat cattggaata tttattatca gttttgttca 2519
cttgttatca gttttgttca ctaatttgc caataatgga attaacgtct tctcatctgt 2579
ttgaggaaga tctgaaacaa ggggccattg caggagtaca tggctccagg cttactttat 2639
atactgctg tatttggtggc tttaaaaaaa tgaccttggt atatgaatgc tttataaata 2699
aataatgcat gaactttaaa aaaaaaaaaa aaa 2732

<210> 61

<211> 399

<212> PRT

<213> Mus musculus

<400> 61

Met	Arg	Ser	Leu	Ser	Leu	Ala	Trp	Leu	Leu	Gly	Gly	Ile	Thr	Leu	Leu
1				5				10						15	
Ala	Ala	Ser	Val	Ser	Cys	Ser	Arg	Thr	Glu	Asn	Leu	Ala	Pro	Gly	Arg
			20					25						30	
Asn	Asn	Ser	Lys	Gly	Arg	Ser	Leu	Ile	Gly	Arg	Leu	Glu	Thr	Gln	Pro
		35					40					45			
Pro	Ile	Thr	Gly	Lys	Gly	Val	Pro	Val	Glu	Pro	Gly	Phe	Ser	Ile	Asp
	50					55					60				
Glu	Phe	Ser	Ala	Ser	Ile	Leu	Thr	Gly	Lys	Leu	Thr	Thr	Val	Phe	Leu
65					70					75					80
Pro	Val	Val	Tyr	Ile	Ile	Val	Phe	Val	Ile	Gly	Leu	Pro	Ser	Asn	Gly
			85						90					95	

Met Ala Leu Trp Ile Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala
 100 105 110
 Val Ile Tyr Met Ala Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile
 115 120 125
 Trp Phe Pro Leu Lys Ile Ser Tyr His Leu His Gly Asn Asn Trp Val
 130 135 140
 Tyr Gly Glu Ala Leu Cys Lys Val Leu Ile Gly Phe Phe Tyr Gly Asn
 145 150 155 160
 Met Tyr Cys Ser Ile Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr
 165 170 175
 Trp Val Ile Val Asn Pro Met Gly His Pro Arg Lys Lys Ala Asn Ile
 180 185 190
 Ala Val Gly Val Ser Leu Ala Ile Trp Leu Leu Ile Phe Leu Val Thr
 195 200 205
 Ile Pro Leu Tyr Val Met Lys Gln Thr Ile Tyr Ile Pro Ala Leu Asn
 210 215 220
 Ile Thr Thr Cys His Asp Val Leu Pro Glu Glu Val Leu Val Gly Asp
 225 230 235 240
 Met Phe Asn Tyr Phe Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro
 245 250 255
 Ala Leu Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Lys Thr Leu Arg
 260 265 270
 Ser Ser Ala Met Asp Glu His Ser Glu Lys Lys Arg Gln Arg Ala Ile
 275 280 285
 Arg Leu Ile Ile Thr Val Leu Ala Met Tyr Phe Ile Cys Phe Ala Pro
 290 295 300
 Ser Asn Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Thr Gln Arg
 305 310 315 320
 Gln Ser His Val Tyr Ala Leu Tyr Leu Val Ala Leu Cys Leu Ser Thr
 325 330 335
 Leu Asn Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser Lys Asp
 340 345 350
 Phe Arg Asp His Ala Arg Asn Ala Leu Leu Cys Arg Ser Val Arg Thr
 355 360 365
 Val Asn Arg Met Gln Ile Ser Leu Ser Ser Asn Lys Phe Ser Arg Lys
 370 375 380
 Ser Gly Ser Tyr Ser Ser Ser Ser Thr Ser Val Lys Thr Ser Tyr
 385 390 395

<210> 62
 <211> 1414
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (50)..(1240)
 <223> C140 receptor, cDNA and deduced protein sequences

<400> 62
 caaagaattg taatagcact cactataggg cgaattcgga tccaggagg atg cgg agc 58
 Met Arg Ser
 1

ccc agc gcg gcg tgg ctg ctg ggg gcc gcc atc ctg cta gca gcc tct 106
 Pro Ser Ala Ala Trp Leu Leu Gly Ala Ala Ile Leu Leu Ala Ala Ser
 5 10 15

ctc tcc tgc agt ggc acc atc caa gga acc aat aga tcc tct aaa gga 154
 Leu Ser Cys Ser Gly Thr Ile Gln Gly Thr Asn Arg Ser Ser Lys Gly
 20 25 30 35

aga agc ctt att ggt aag gtt gat ggc aca tcc cac gtc act gga aaa 202
 Arg Ser Leu Ile Gly Lys Val Asp Gly Thr Ser His Val Thr Gly Lys
 40 45 50

gga gtt aca gtt gaa aca gtc ttt tct gtg gat gag ttt tct gca tct 250
 Gly Val Thr Val Glu Thr Val Phe Ser Val Asp Glu Phe Ser Ala Ser
 55 60 65

gtc ctc gct gga aaa ctg acc act gtc ttc ctt cca att gtc tac aca 298
 Val Leu Ala Gly Lys Leu Thr Thr Val Phe Leu Pro Ile Val Tyr Thr
 70 75 80

att gtg ttt gcg gtg ggt ttg cca agt aac ggc atg gcc cta tgg gtc 346
 Ile Val Phe Ala Val Gly Leu Pro Ser Asn Gly Met Ala Leu Trp Val
 85 90 95

ttt ctt ttc cga act aag aag aag cac cct gct gtg att tac atg gcc 394
 Phe Leu Phe Arg Thr Lys Lys Lys His Pro Ala Val Ile Tyr Met Ala
 100 105 110 115

aat ctg gcc ttg gct gac ctc ctc tct gtc atc tgg ttc ccc ttg aag 442
 Asn Leu Ala Leu Ala Asp Leu Leu Ser Val Ile Trp Phe Pro Leu Lys
 120 125 130

att gcc tat cac ata cat ggc aac aac tgg att tat ggg gaa gct ctt 490
 Ile Ala Tyr His Ile His Gly Asn Asn Trp Ile Tyr Gly Glu Ala Leu
 135 140 145

tgt aat gtg ctt att ggc ttt ttc tat cgc aac atg tac tgt tcc att 538
 Cys Asn Val Leu Ile Gly Phe Phe Tyr Gly Asn Met Tyr Cys Ser Ile
 150 155 160

ctc ttc atg acc tgc ctc agt gtg cag agg tat tgg gtc atc gtg aac 586
 Leu Phe Met Thr Cys Leu Ser Val Gln Arg Tyr Trp Val Ile Val Asn
 165 170 175

ccc atg ggg cac tcc agg aag aag gca aac att gcc att ggc atc tcc	634
Pro Met Gly His Ser Arg Lys Lys Ala Asn Ile Ala Ile Gly Ile Ser	
180 185 190 195	
ctg gca ata tgg ctg ctg act ctg ctg gtc acc atc cct ttg tat gtc	682
Leu Ala Ile Trp Leu Leu Thr Leu Leu Val Thr Ile Pro Leu Tyr Val	
200 205 210	
gtg aag cag acc atc ttc att cct gcc ctg aac atc acg acc tgt cat	730
Val Lys Gln Thr Ile Phe Ile Pro Ala Leu Asn Ile Thr Thr Cys His	
215 220 225	
gat gtt ttg cct gag cag ctc ttg gtg gga gac atg ttc aat tac ttc	778
Asp Val Leu Pro Glu Gln Leu Leu Val Gly Asp Met Phe Asn Tyr Phe	
230 235 240	
ctc tct ctg gcc att ggg gtc ttt ctg ttc cca gcc ttc ctc aca gcc	826
Leu Ser Leu Ala Ile Gly Val Phe Leu Phe Pro Ala Phe Leu Thr Ala	
245 250 255	
tct gcc tat gtg ctg atg atc aga atg ctg cga tct tct gcc atg gat	874
Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser Ala Met Asp	
260 265 270 275	
gaa aac tca gag aag aaa agg aag agg gcc atc aaa ctc att gtc act	922
Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu Ile Val Thr	
280 285 290	
gtc ctg ggc atg tac ctg atc tgc ttc act cct agt aac ctt ctg ctt	970
Val Leu Gly Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn Leu Leu Leu	
295 300 305	
gtg gtg cat tat ttt ctg att aag agc cag ggc cag agc cat gtc tat	1018
Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser His Val Tyr	
310 315 320	
gcc ctg tac att gta gcc ctc tgc ctc tct acc ctt aac agc tgc atc	1066
Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn Ser Cys Ile	
325 330 335	
gac ccc ttt gtc tat tac ttt gtt tca cat gat ttc agg gat cat gca	1114
Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg Asp His Ala	
340 345 350 355	
aag aac gct ctc ctt tgc cga agt gtc cgc act gta aag cag atg caa	1162
Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys Gln Met Gln	
360 365 370	
gta ccc ctc acc tca aag aaa cac tcc agg aaa tcc agc tct tac tct	1210
Val Pro Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser Ser Tyr Ser	
375 380 385	
tca agt tca acc act gtt aag acc tcc tat tgagttttcc aggtcctcag	1260
Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr	
390 395	
atgggaattg cacagtagga tgtggaacct gtttaatggt atgaggacgt gtctggttatt	1320

tccggatcca gatcttatta aagcagaact tgtttattgc agcttataat ggttacaaat 1380
aaagcaatag catcacaaat ttcacaaata aagc 1414

<210> 63
<211> 397
<212> PRT
<213> Homo sapiens

<400> 63

Met	Arg	Ser	Pro	Ser	Ala	Ala	Trp	Leu	Leu	Gly	Ala	Ala	Ile	Leu	Leu	
1				5					10					15		
Ala	Ala	Ser	Leu	Ser	Cys	Ser	Gly	Thr	Ile	Gln	Gly	Thr	Asn	Arg	Ser	
			20					25					30			
Ser	Lys	Gly	Arg	Ser	Leu	Ile	Gly	Lys	Val	Asp	Gly	Thr	Ser	His	Val	
		35					40					45				
Thr	Gly	Lys	Gly	Val	Thr	Val	Glu	Thr	Val	Phe	Ser	Val	Asp	Glu	Phe	
	50					55					60					
Ser	Ala	Ser	Val	Leu	Ala	Gly	Lys	Leu	Thr	Thr	Val	Phe	Leu	Pro	Ile	
65					70					75					80	
Val	Tyr	Thr	Ile	Val	Phe	Ala	Val	Gly	Leu	Pro	Ser	Asn	Gly	Met	Ala	
				85					90					95		
Leu	Trp	Val	Phe	Leu	Phe	Arg	Thr	Lys	Lys	Lys	His	Pro	Ala	Val	Ile	
		100						105					110			
Tyr	Met	Ala	Asn	Leu	Ala	Leu	Ala	Asp	Leu	Leu	Ser	Val	Ile	Trp	Phe	
	115						120					125				
Pro	Leu	Lys	Ile	Ala	Tyr	His	Ile	His	Gly	Asn	Asn	Trp	Ile	Tyr	Gly	
	130					135					140					
Glu	Ala	Leu	Cys	Asn	Val	Leu	Ile	Gly	Phe	Phe	Tyr	Gly	Asn	Met	Tyr	
145				150						155					160	
Cys	Ser	Ile	Leu	Phe	Met	Thr	Cys	Leu	Ser	Val	Gln	Arg	Tyr	Trp	Val	
				165					170					175		
Ile	Val	Asn	Pro	Met	Gly	His	Ser	Arg	Lys	Lys	Ala	Asn	Ile	Ala	Ile	
		180						185					190			
Gly	Ile	Ser	Leu	Ala	Ile	Trp	Leu	Leu	Thr	Leu	Leu	Val	Thr	Ile	Pro	
	195						200					205				
Leu	Tyr	Val	Val	Lys	Gln	Thr	Ile	Phe	Ile	Pro	Ala	Leu	Asn	Ile	Thr	
	210					215					220					
Thr	Cys	His	Asp	Val	Leu	Pro	Glu	Gln	Leu	Leu	Val	Gly	Asp	Met	Phe	
225					230					235				240		
Asn	Tyr	Phe	Leu	Ser	Leu	Ala	Ile	Gly	Val	Phe	Leu	Phe	Pro	Ala	Phe	
			245						250					255		

Leu Thr Ala Ser Ala Tyr Val Leu Met Ile Arg Met Leu Arg Ser Ser
 260 265 270
 Ala Met Asp Glu Asn Ser Glu Lys Lys Arg Lys Arg Ala Ile Lys Leu
 275 280 285
 Ile Val Thr Val Leu Gly Met Tyr Leu Ile Cys Phe Thr Pro Ser Asn
 290 295 300
 Leu Leu Leu Val Val His Tyr Phe Leu Ile Lys Ser Gln Gly Gln Ser
 305 310 315 320
 His Val Tyr Ala Leu Tyr Ile Val Ala Leu Cys Leu Ser Thr Leu Asn
 325 330 335
 Ser Cys Ile Asp Pro Phe Val Tyr Tyr Phe Val Ser His Asp Phe Arg
 340 345 350
 Asp His Ala Lys Asn Ala Leu Leu Cys Arg Ser Val Arg Thr Val Lys
 355 360 365
 Gln Met Gln Val Pro Leu Thr Ser Lys Lys His Ser Arg Lys Ser Ser
 370 375 380
 Ser Tyr Ser Ser Ser Ser Thr Thr Val Lys Thr Ser Tyr
 385 390 395